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L7 and PCR | 59

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Database:

L7 and PCR

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USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L7 and PCR	59	<u>L9</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L7 and thermo?	0	<u>L8</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and tyrosine and substitut?	66	<u>L7</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and tyrosine	326	<u>L6</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and YxGG/A?	0	<u>L5</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and Y-GG/A?	0	<u>L4</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and Yx-gga?	0	<u>L3</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	L1 and GG/A?	0	<u>L2</u>
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	DNA adj polymerase?	1837	<u>L1</u>

 **PALM INTRANET**

Day : Tuesday
Date: 10/23/2001
Time: 15:07:43

Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.

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 NEWS 17 Oct 22 Over 1 million reactions added to CASREACT
 NEWS 18 Oct 22 DGENE GETSIM has been improved

NEWS EXPRESS August 15 CURRENT WINDOWS VERSION IS V6.0C,
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=> s DNA adj polymerase
L1 0 DNA ADJ POLYMERASE

=> s polymerase?
L2 712554 POLYMERASE?

=> s DNA?(a)polymerase
L3 91094 DNA?(A) POLYMERASE

=> s DNA?(a)polymerase?
L4 91103 DNA?(A) POLYMERASE?

=> s l4 and B?
TERM 'B?' EXCEEDED TRUNCATION LIMITS - SEARCH ENDED
1 FILES SEARCHED...

<-----User Break----->

u

SEARCH ENDED BY USER

You have entered a truncated stem which occurs in too many terms.
Make the stem longer and try again. For example, if your original
term was 'degr?' to search for variations and the abbreviation for
'degradation', you could replace it with the expression '(degrdn OR
degrad?)'. If your search term was numeric, e.g., 'C>5', reduce the
size of the range.

=> s l4 and (b-type)
L5 145 L4 AND (B-TYPE)

=> s l4 and B-type?
L6 145 L4 AND B-TYPE?

=> s l4 and B-?
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION

ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
ADDITIONAL CHARACTERS REQUIRED AFTER '?' FOR LEFT TRUNCATION
Additional characters must follow the left truncation symbol in your search term. If your search term contains a punctuation mark before the truncation symbol and you are searching in a field that uses implied proximity, the system may interpret the truncation symbol as being at the beginning of a term. Implied proximity is used in search fields indexed as single words, for example, the Basic Index. To see which fields in the current file have left truncation, enter "HELP SFIELDS" at an arrow prompt (=>).

=> s 16 and exonuclease?
L7 28 L6 AND EXONUCLEASE?

=> s 16 and polymerase?
L8 145 L6 AND POLYMERASE?

=> s 16 and Y-GG?A?
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'GG?A?'

The truncation symbol ? may be used only at the end of a search term. To specify a variable character within a word use '!!', e.g., 'wom!!n' to search for both 'woman' and 'women'. Enter "HELP TRUNCATION" at an arrow prompt (=>) for more information.

=> s 16 and Y-GG/A?
'A?' IS NOT A VALID FIELD CODE
L9 0 L6 AND Y-GG/A?

=> s 16 and gga?
L10 0 L6 AND GGA?

=> s 16 and y?
4 FILES SEARCHED...
<-----User Break----->
u
SEARCH ENDED BY USER

=> d history

(FILE 'HOME' ENTERED AT 13:01:13 ON 23 OCT 2001)

FILE 'MEDLINE, EMBASE, CAPLUS, SCISEARCH, BIOSIS, REGISTRY' ENTERED AT
13:01:33 ON 23 OCT 2001

L1 0 S DNA ADJ POLYMERASE
L2 712554 S POLYMERASE?
L3 91094 S DNA?(A) POLYMERASE?
L4 91103 S DNA?(A) POLYMERASE?
L5 145 S L4 AND (B-TYPE)
L6 145 S L4 AND B-TYPE?

L7 28 S L6 AND EXONUCLEASE?
L8 145 S L6 AND POLYMERASE?
L9 0 S L6 AND Y-GG/A?
L10 0 S L6 AND GGA?

=> dup rem 17
DUPLICATE IS NOT AVAILABLE IN 'REGISTRY'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L7
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=> dup rem 17
DUPLICATE IS NOT AVAILABLE IN 'REGISTRY'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L7
COMMAND INTERRUPTED
If this message appears repeatedly, please notify the Help Desk.
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Desk by telephone or via SEND in the STNMAIL file.

=> s 17 and PCR
L13 7 L7 AND PCR

=> dup rem 113
DUPLICATE IS NOT AVAILABLE IN 'REGISTRY'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L13
L14 4 DUP REM L13 (3 DUPLICATES REMOVED)

=> d 114 ibib abs 1-
YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:676310 CAPLUS
DOCUMENT NUMBER: 135:237584
TITLE: Methods of making mutant **B-type**
DNA polymerases from Thermococcus
aggregans with improved performance in PCR
INVENTOR(S): Sobek, Harald; Frey, Bruno; Antranikian, Garabed;
Boehlke, Kristina; Pisani, Francesca Maria; Rossi,
Mose
PATENT ASSIGNEE(S): Roche Diagnostics G.m.b.H., Germany
SOURCE: Eur. Pat. Appl., 40 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1132474	A1	20010912	EP 2001-1104583	20010306
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001269188	A2	20011002	JP 2001-61781	20010306
PRIORITY APPLN. INFO.:			EP 2000-105155	A 20000311
AB The invention provides methods of making mutant B-type				

important factor for the equilibrium between DNA polymerisation and exonucleolysis.

L14 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 2
ACCESSION NUMBER: 2000:762603 CAPLUS
DOCUMENT NUMBER: 134:322588
TITLE: PCR performance of the **B**-type DNA polymerase from the thermophilic euryarchaeon *Thermococcus aggregans* improved by mutations in the Y-GG/A motif
AUTHOR(S): Bohike, Kristina; Pisani, Francesca M.; Vorgias, Constantinos E.; Frey, Bruno; Sobek, Harald; Rossi, Mose; Antranikian, Garabed
CORPORATE SOURCE: Institute of Technical Microbiology, Technical University Hamburg-Harburg, Hamburg, 21073, Germany
SOURCE: Nucleic Acids Res. (2000), 28(20), 3910-3917
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The effect of mutations in the highly conserved Y-GG/A motif of **B**-type DNA polymerases was studied in the **DNA polymerase** from the hyperthermophilic euryarchaeon *Thermococcus aggregans*. This motif plays a crit. role in the balance between the synthesis and degrdn. of the DNA chain. Five different mutations of the tyrosine at position 387 (Tyr387.fwdarw.Phe, Tyr387.fwdarw.Trp, Tyr387.fwdarw.His, Tyr387.fwdarw.Asn and Tyr387.fwdarw.Ser) revealed that an arom. ring system is crucial for the synthetic activity of the enzyme. Amino acids at this position lacking the ring system (Ser and Asn) led to a significant decrease in polymerase activity and to enhanced **exonuclease** activity, which resulted in improved enzyme fidelity. Exchange of tyrosine to phenylalanine, tryptophan or histidine led to phenotypes with wild-type-like fidelity
but enhanced PCR performance that could be related to a higher velocity of polymn. With the help of a modeled structure of *T. aggregans* **DNA polymerase**, the biochem. data were interpreted proposing that the conformation of the flexible loop contg. the Y-GG/A motif is an important factor for the equil. between DNA polymn. and exonucleolysis.
REFERENCE COUNT: 37
REFERENCE(S):
(1) Barnes, W; Proc Natl Acad Sci 1994, V91, P2216 CAPLUS
(2) Bult, C; Science 1996, V273, P1058 CAPLUS
(4) Cann, I; J Bacteriol 1999, V181, P5984 CAPLUS
(5) Cann, I; Proc Natl Acad Sci 1998, V95, P14250 CAPLUS
(6) Dong, Q; J Biol Chem 1993, V268, P24163 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:354514 CAPLUS
DOCUMENT NUMBER: 131:154392
TITLE: Molecular cloning, sequence and expression of Aa-polB,
a mitochondrial gene encoding a family B DNA polymerase from the edible basidiomycete *Agrocybe aegerita*
AUTHOR(S): Bois, F.; Barroso, G.; Gonzalez, P.; Labarere, J.
CORPORATE SOURCE: Laboratoire de Genetique Moleculaire et d'Amelioration

des Champignons Cultives, CRA de Bordeaux, Villenave d'Ornon Cedex, F-33883, Fr.
SOURCE: Mol. Gen. Genet. (1999), 261(3), 508-513
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB An ORF of 1716 nucleotides, putatively encoding a **DNA polymerase**, was characterized in the mitochondrial genome of the edible basidiomycete *Agrocybe aegerita*. The complete gene, named Aa-polB, and its flanking regions were cloned and sequenced from three overlapping restriction fragments. Aa-polB is located between the SSU rDNA (5' region) and a gene for tRNA Asn (3' region), and is sep'd. from these genes by two A +T-rich intergenic regions of 1048 (5' region) and 3864 (3' region) nucleotides, which lack repeated sequences of mitochondrial or plasmid origin. The deduced Aa-POLB protein shows extensive sequence similarity with the family B **DNA polymerases** encoded by genomes that rely on protein-primed replication (invertrons). The domains involved in the 3'.fwdarw.5' **exonuclease** (Exo I to III) and polymerase (Pol I to Pol V) activities were localized on the basis of conserved sequence motifs. The alignment of the Aa-POLB protein (571 amino acids) with sequences of family B **DNA polymerases** from invertrons revealed that in Aa-POLB the N-terminal region preceding Exo I is short, suggesting a close relationship with the **DNA polymerases** of bacteriophages that have linear DNA. The Aa-polB gene was shown to be present in all wild strains examd., which were collected from a wide range of locations in Europe. As shown by RT-PCR, the Aa-polB gene is transcribed in the mitochondria, at a low but significant level. The likelihood of the coexistence of Aa-POLB and Pol .gamma. in the *A. aegerita* mitochondrion is discussed in the light of recent reports showing the conservation of the nucleus-encoded Pol .gamma.
from yeast to human.

REFERENCE COUNT: 28
REFERENCE(S): (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Barroso, G; Appl Environ Microbiol 1995, V61, P1187 CAPLUS
(3) Blanco, L; Gene 1991, V100, P27 CAPLUS
(6) Coleman, A; J Protozool 1991, V38, P129 CAPLUS
(7) Dohmen, G; Curr Genet 1994, V25, P59 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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---Logging off of STN---

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